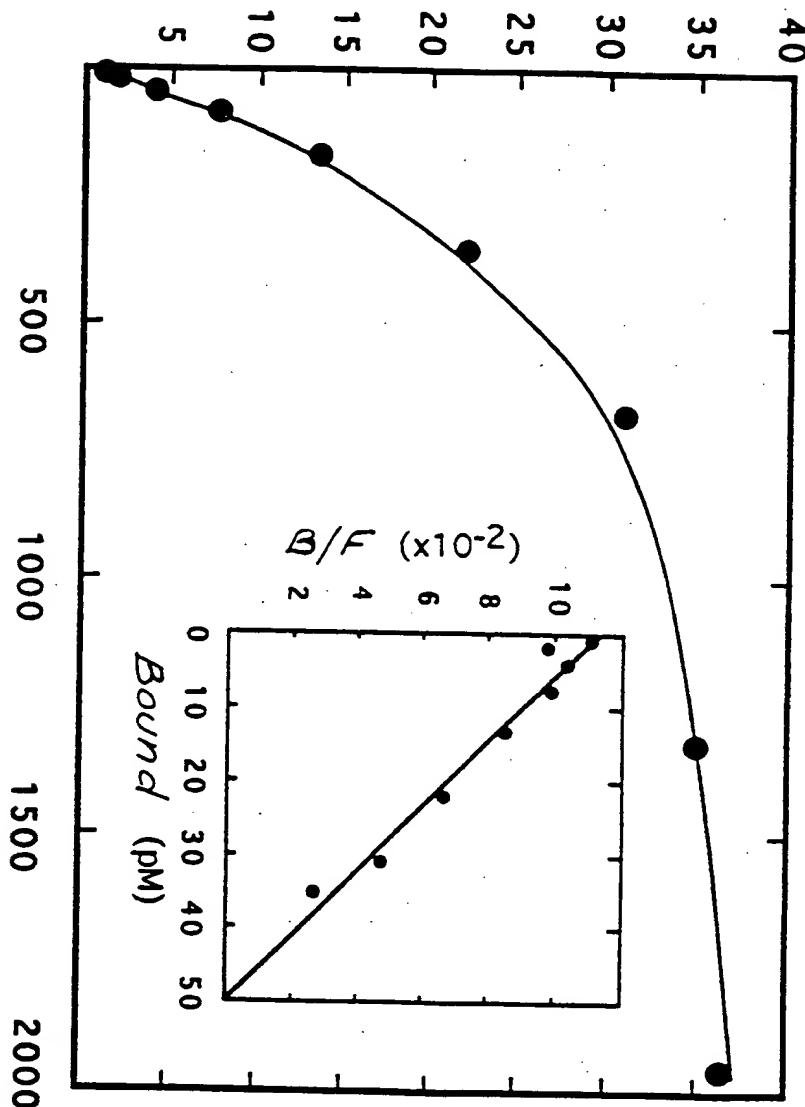


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95/4
09/077817

1/19

[¹²⁵I]-IL-13 Bound (pM)



[¹²⁵I]-IL-13 (pM)

FIG. 1a

09/07/817

2/19

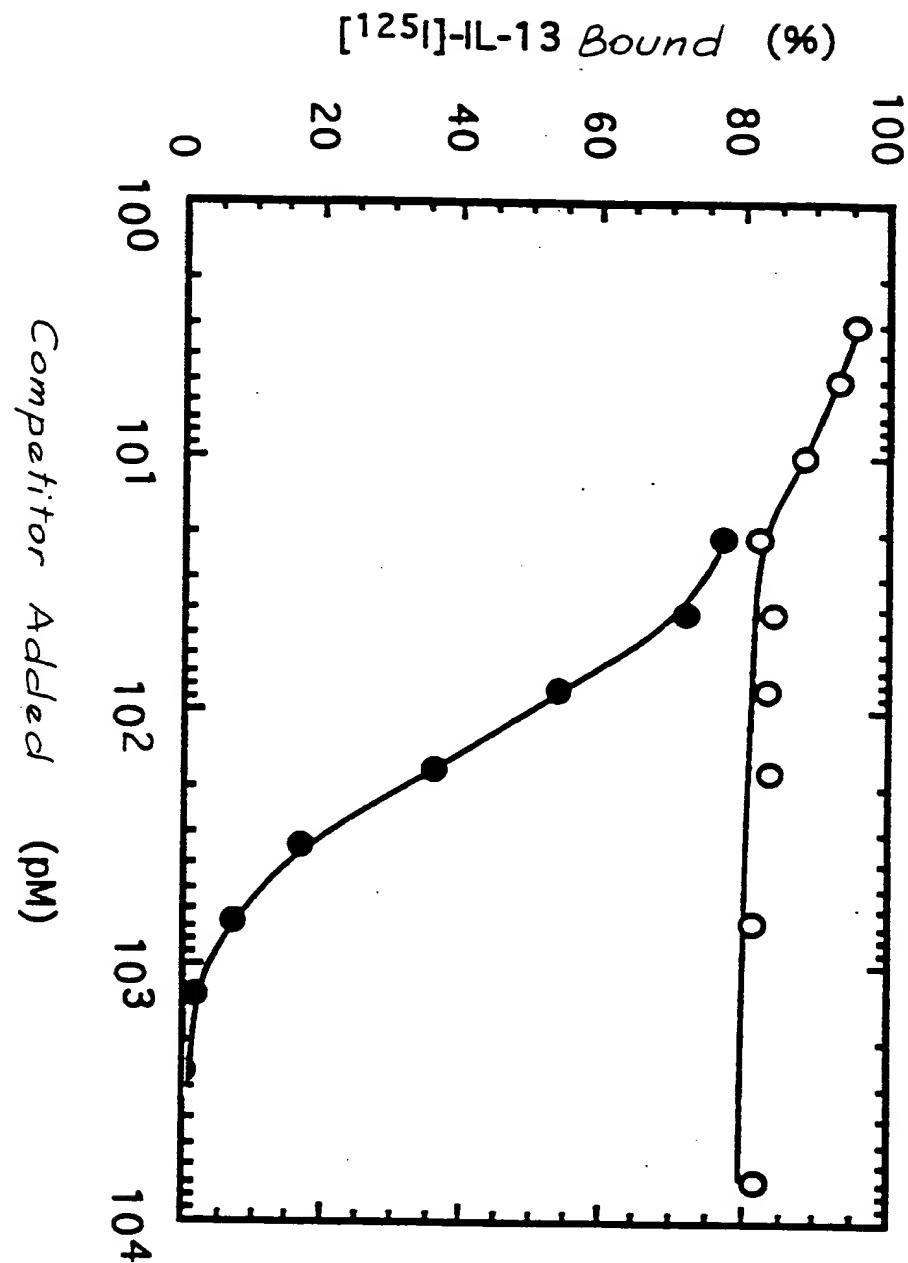


FIG. 1b

09/077817

3/19

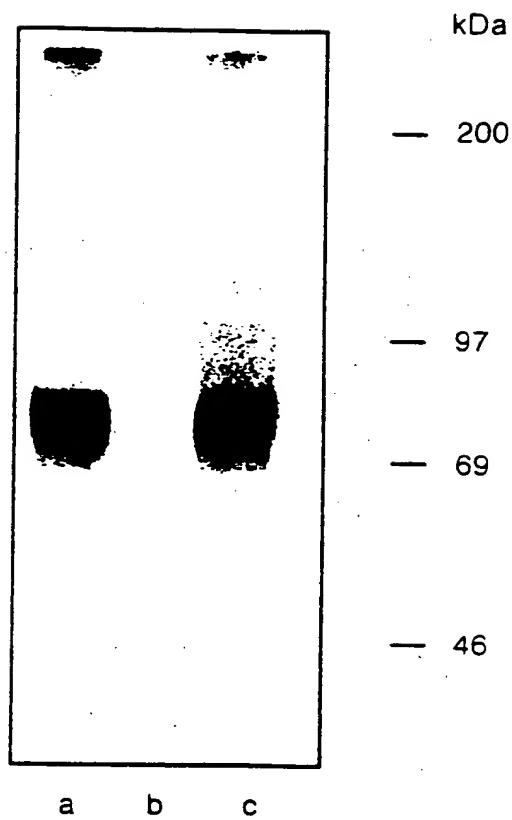


FIG. 1c

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4/19

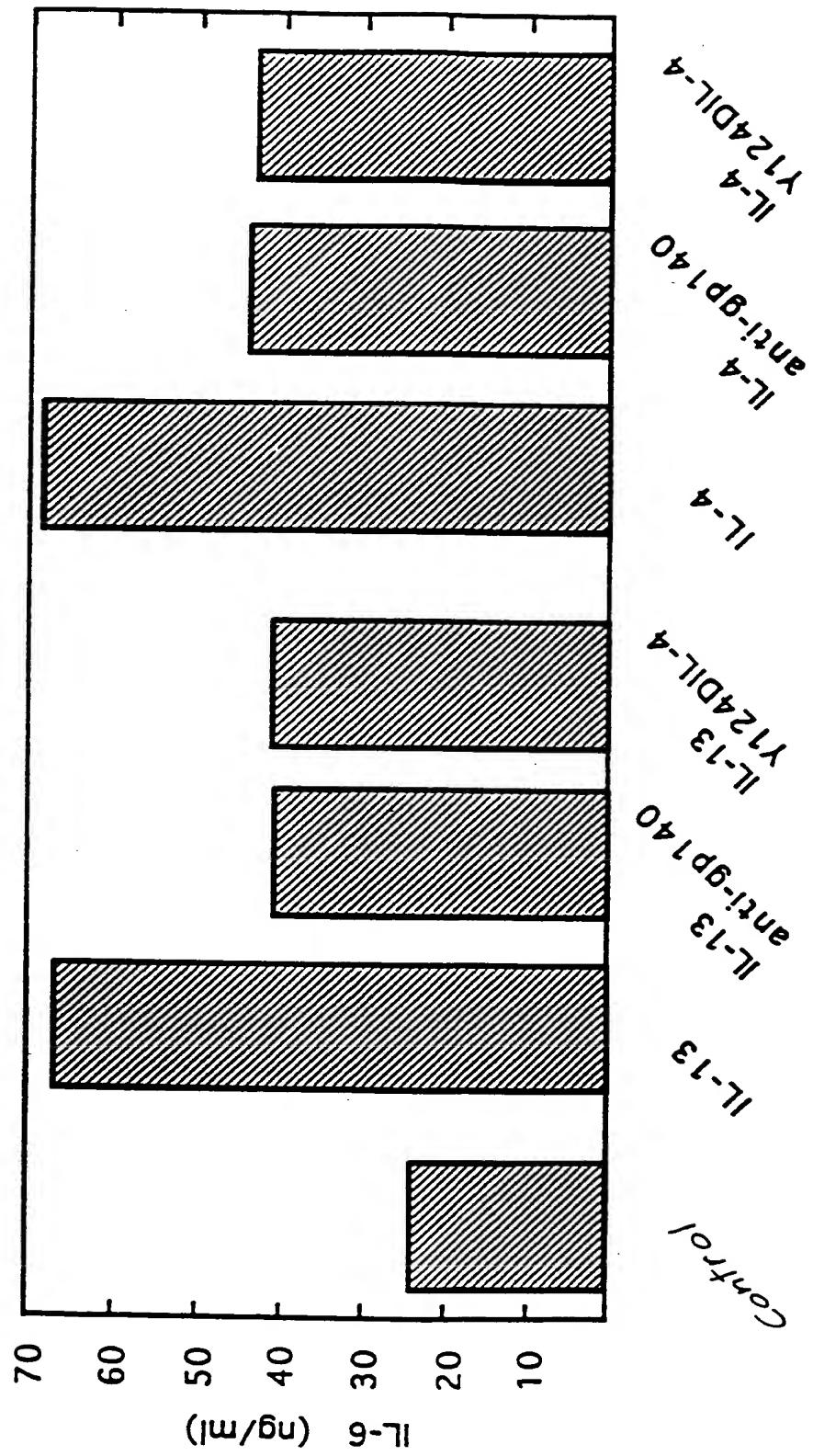


FIG. 1D

1	GGTGCCTGGGGAGAGGCAATATCAAGGTTAAATCTGGAGAAATGGCT	58
1	MetAla	2
59	TTCGTTGCTGGCTATGGATGCTTACCTTCTGATAAGCACACATTGGCT	118
3	PheValCysLeuAlaIleGlyCysLeuTyrrThrPheLeuIleSerThrPheGlyCys	22
119	ACTTCATCTTCAGACACCCGAGATAAAAGTTAACCTCCCTCAGGATTTGAGATACTGGAT	178
23	ThrSerSerAspThrGluIleLeuValAlaSerProProGlnAspPheGluIleValAsp	42
179	CCGGATACCTAGCTTATCTCTATTGCAATGGCAACCCCCACTGTCTGGATCATTT	238
43	ProGlyTyrIleGlyTyrIleLeuTyrrLeuGlnTrpGlnProProLeuSerLeuAspHisPhe	62
239	AAGGAATGGCACAGTGAATATGAACTAAATACCGAAACATTGGTAGTGAACATGGAAAG	298
63	LysGluCysThrValGluTyrrGluLeuLysTyrArgAsnIleGlySerGluThrTrpLys	82
299	ACCATCATTAGAACATTACATTACAAAGATGGGTTGATCTTAACAAAGGGATTGAA	358
83	ThrIleThrLysAsnLeuHisTyrrLysAspGlyPheAspLeuAsnLysGlyIleGlu	102
359	GCGAAGATAACACGCTTTACCATGGCAATGGATCAGAAAGTCAAGTCC	418
103	AlaLysIleHisThrLeuLeuProTrpGlnCysThrAsnGlySerGluValGlnSerSer	122
419	TGGGCAGAAACTATTGGATATCACCAAGGAATTCCAGAAACTAAAGTCAGGAT	478
123	TrpAlaGluThrThrIleSerProGlnGlyIleProGluThrLysValGlnAsp	142
479	ATGGATTGGCTATTACAAATTACTCTGTTACTGGTATGAGGCTTGGATCATGCATT	538
143	MetAspCysValTyrItyrasnTrpGlnTyrrLeuCysSerTrpLysProGlyIleGly	162
539	GTAACCTCTGCTGATACATCAAGGCAATTGGAAATAGGATGGCAGATTCCCTATTTG	598
163	ValLeuLeuAspThrAsnTyrrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu	182
599	CAGTGTGTTGATGGCTGATGGACAAATATAGGATGGCAGATTCCCTATTTG	658
183	GlnCysValAspTyrIleLeuAlaAspGlyGlnAsnIleGlyCysArgPheProTyrLeu	202

5/19

09/077817

FIG. 2a

09/077817

6/19

659	GAGGCATCAGACTATAAGATTCTATATTGGATCATCAGAGAACAGCCT	718
203	GluAlaSerAspTyrLysAspPheTyrIleCysValAlaGlySerSerGluAsnLyAspPro	222
719	ATCAGATCCAGTTACTTTCAAGCTCAAAATATAGTTAACCTTTCGCCGCCAGTC	778
223	IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleValIleValIleAspProLeuProProVal	242
779	TATCTTACTTTACTCGGGAGAGTTCATGTGAAATTAAAGCTGAAATGGAGCATAACCTTGC	838
243	TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuIleTrpSerIleProLeu	262
839	GGACCTATTCCAGCAAAGGTGTTGATTATGAAATTGAGATCAGGAAAGATGATACTACC	898
263	GlyProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspAspThrThr	282
899	TTGGTGAATGCTACAGTGTAAATGAAACATACACCTTGAAGAACAAATGAAACCGA	958
283	LeuValThrAlaThrValGluAsnGluThrTyrThrLeuIleThrAsnGluIleThrArg	302
959	CAATTATGCTTTGTAGTAAGGAAAGTGAATATTGAACTTGTCAAGATGACGGAAATTGG	1018
303	GlnLeucyAspHeValValArgSerIleValAsnIleTyrCysSerAspAspGlyIleTrp	322
1019	AGTGAGTGGAGGTGATAAACAAATGGCTGGAAAGGTGAAGAACCTATCGAAGAAACCTTTGCTA	1078
323	SerGluTrpSerAspLysGlnCysTrpGluGlyGluAspLeuSerLysThrLeuLeu	342
1079	CGTTCTGGCTACCATTTGGTTCATCTTAATATTAGTTATATTGTAACCGGGTCTGCTT	1138
343	ArgPheTrpLeuProPheGlyPheIleLeuValIleLeuValIlePheValThrGlyLeuLeu	362
1139	TTGCGTAAAGCCAAACACCTACCCAAAATGATTCCAGAATTCTGTGATACATGAGA	1198
363	LeuIleArgLysProAsnThrIleProLysMetIleProGluPhePheCysAspThr	381
1199	CTTCCATATCAAGAGACATGGTATGACTCAACAGTTCCAGTCATGCCAAATGTCA	1258
1259	ATATGAGTCTCATAAACTGAATTCTTCTTGGAAATGTTG 1298	

FIG. 2 a (continuation)

09/077817

7/19

IL13R MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGLY 50
IL5R ..MIIVAHVLLILLGATEILQADLLPDEKISLLPPVNFTIKVTG.LAQVL 47

IL13R LQWQPPPLSLDHFKECTVEYELKVRNIGSETWKTIIITKNLHYKDGFDLNKG 100
IL5R LQWKPNPDQEQ.RNVNLEYQVKINAPKEDDYETRITES...KCVTILHKG 93

IL13R IEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV.... 146
IL5R FSASVRTILQ...NDHSLLASSWASAE.LHAPPGSPGTSIVNLTCTTNTT 139

IL13R ..YYNWQ.....YLLOSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK 189
IL5R EDNYSRLRSYQVSILQITWLVGTDAPEDTQYFLYYRYGSWTE..EQEYSK 187

IL13R AD.GQNIGORFP..YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIV 236
IL5R DTLGRNIAQWFPRTFILSKGRDWLSVLVNGSSKHSAIRPDFQFLALHAID 237

IL13R KPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTLVTA 286
IL5R QINPPLNVTAEIEGT.RLSIQWEKPVSAFPPIHCFDYEVKIHNTRNGYLQI 286

IL13R TVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDL 336
IL5R EKLMTNAFISIIDDLSKYDVQVRAAVSSMCREAGLWSEWSQ.PIYVGND 335

IL13R SKKTLLRFWLPFGFILILVIFVTGLLLRKPNTPKMIP.....EF 376
IL5R HKPLREWFVIVIMATICFILLILSLICKICHLWIKLFPPIPAPKSNIKDL 385

IL13R FCDT..... 380
IL5R FVTNYEKAGSSETIEVICYIEKPGVETLEDVF 420

FIG. 2b

09/077817

8/19

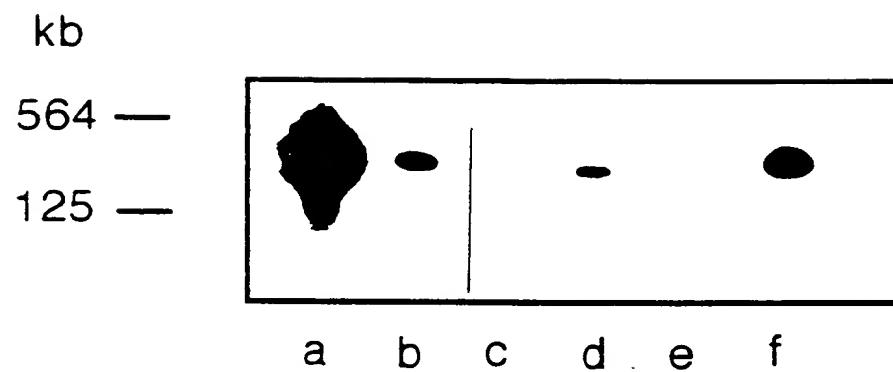


FIG. 3

09/077817

9/19

[^{125}I]-IL-13 Bound (pM)

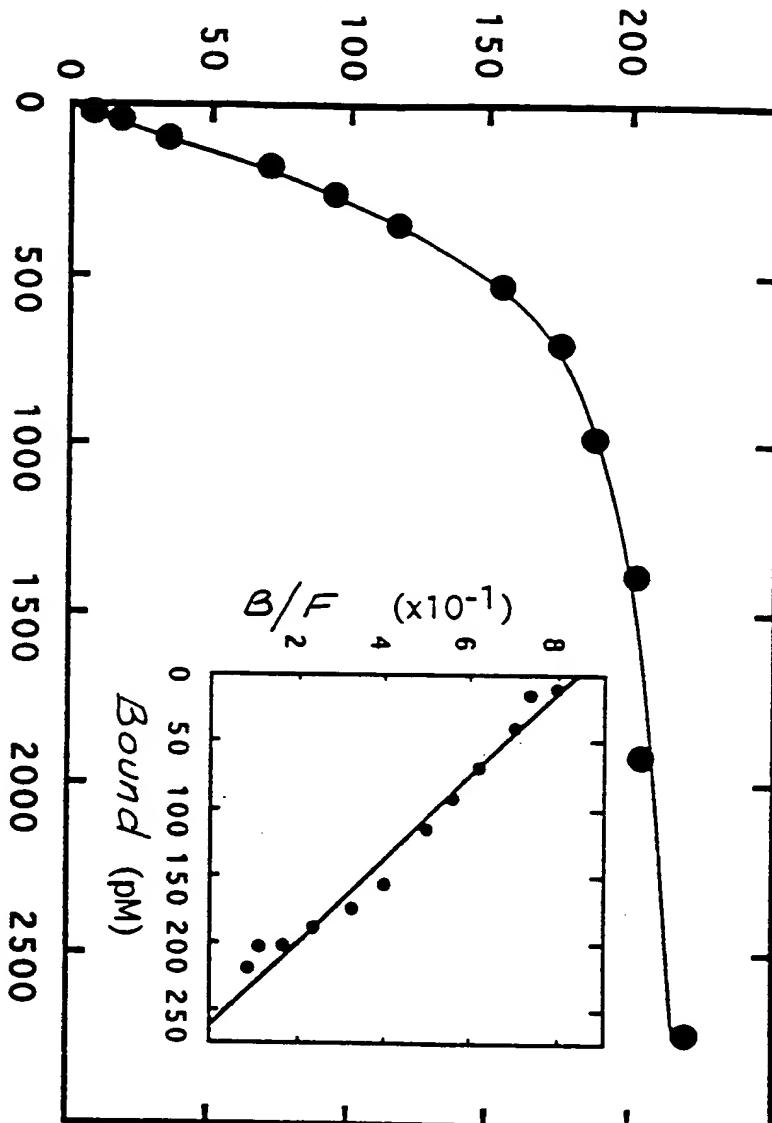


FIG. 4a

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09/077817

10/19

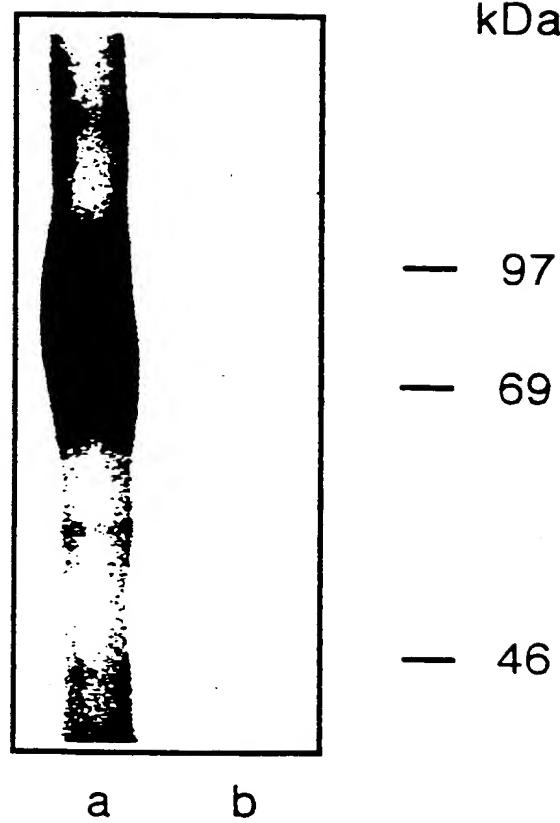


FIG.4b

09/077817

11/19

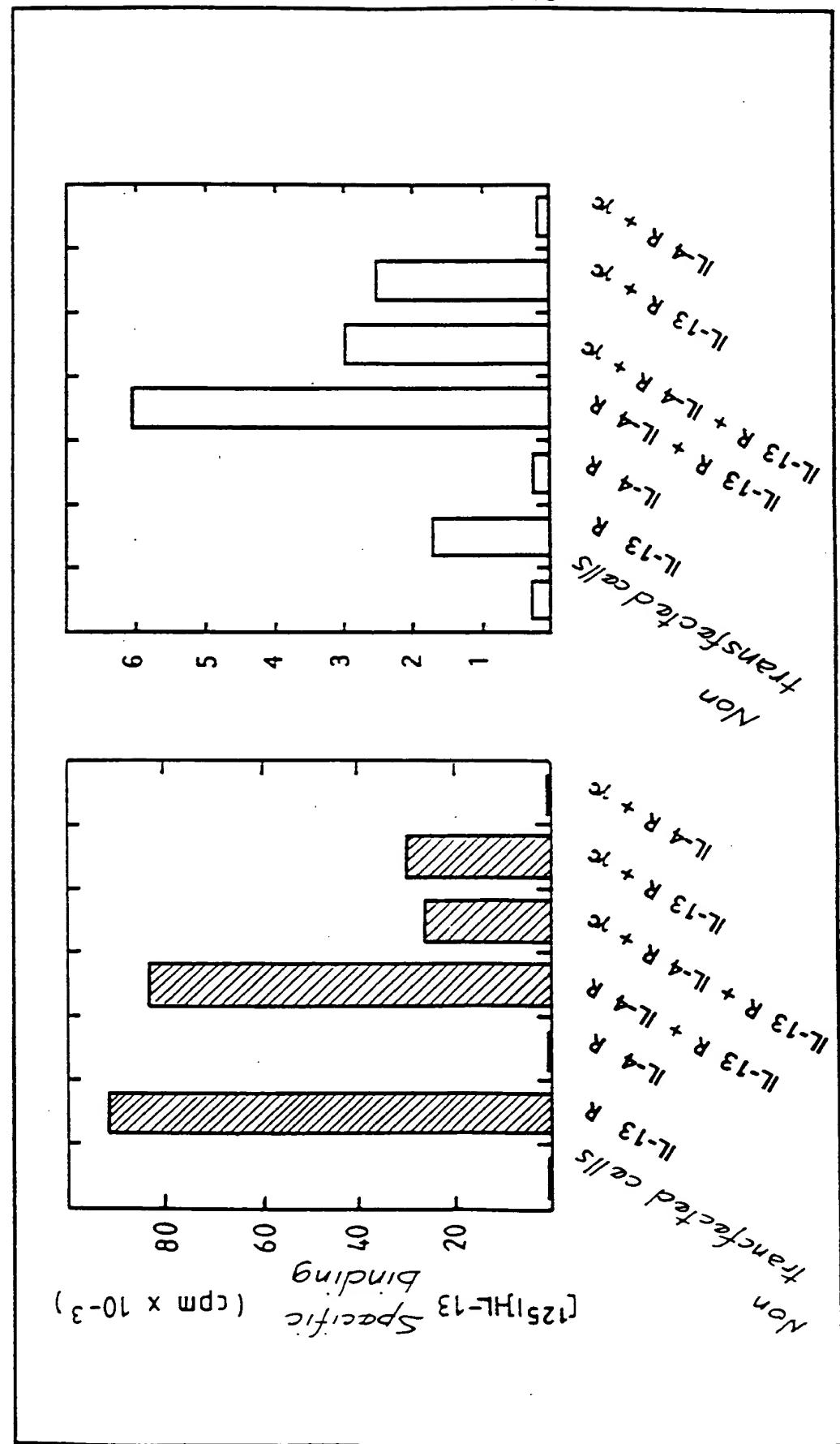


FIG. 4C

09/077817

12/19

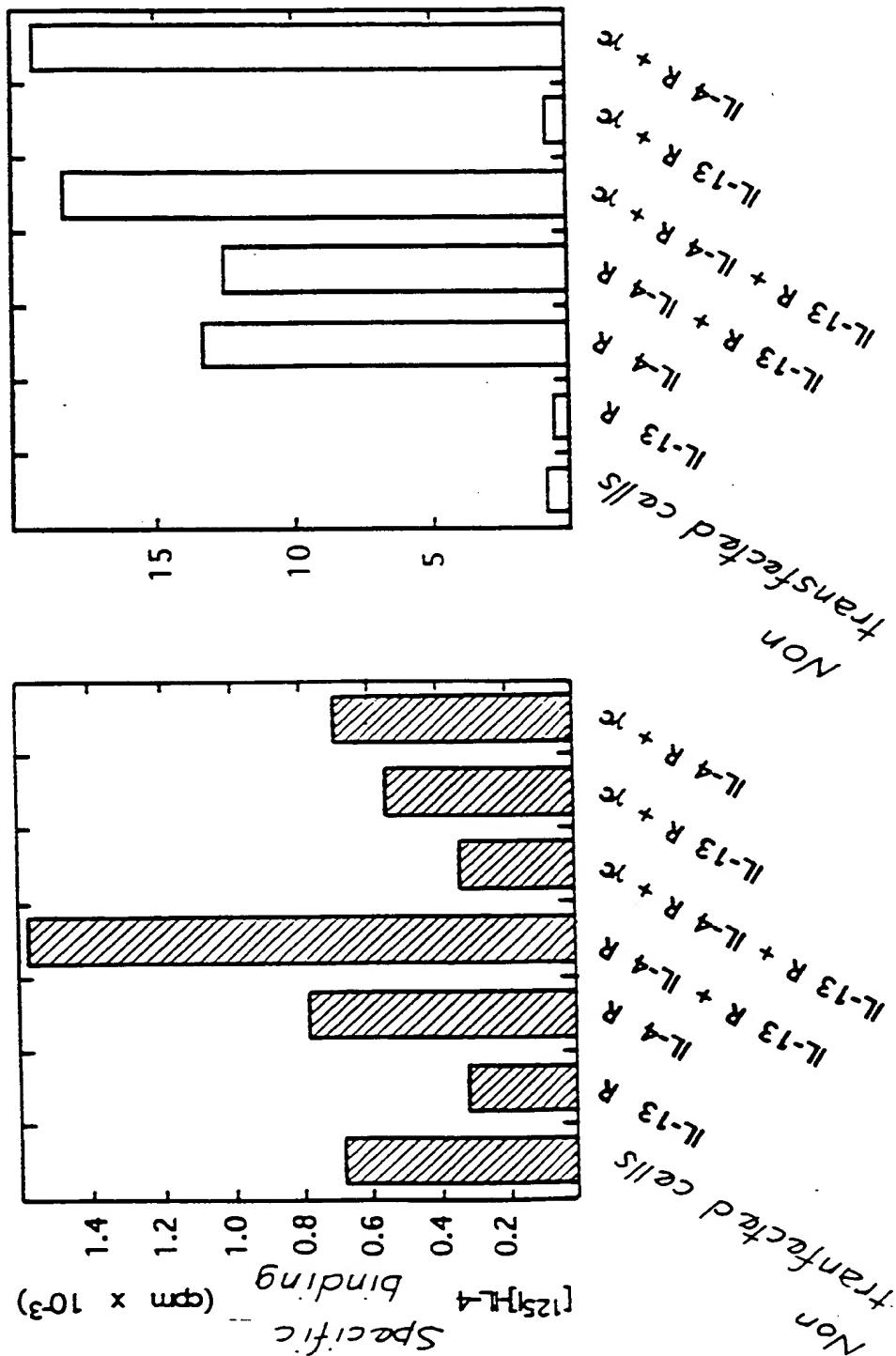


FIG. 4.d

09/07/817

13/19

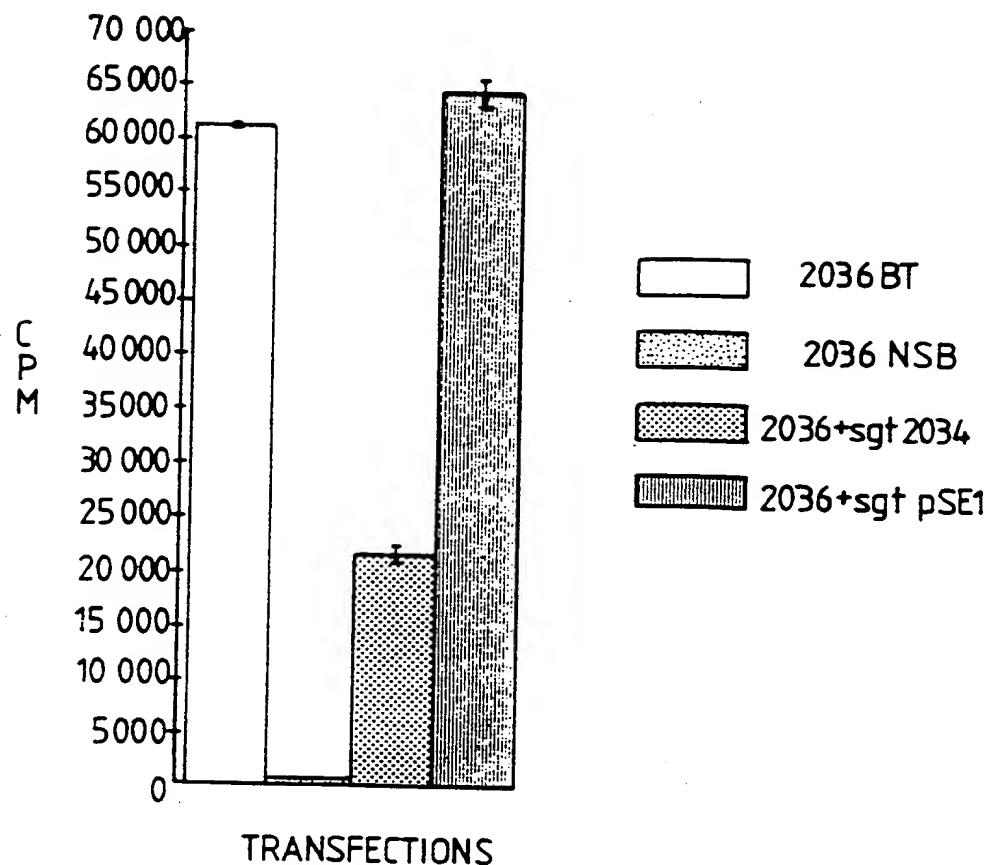
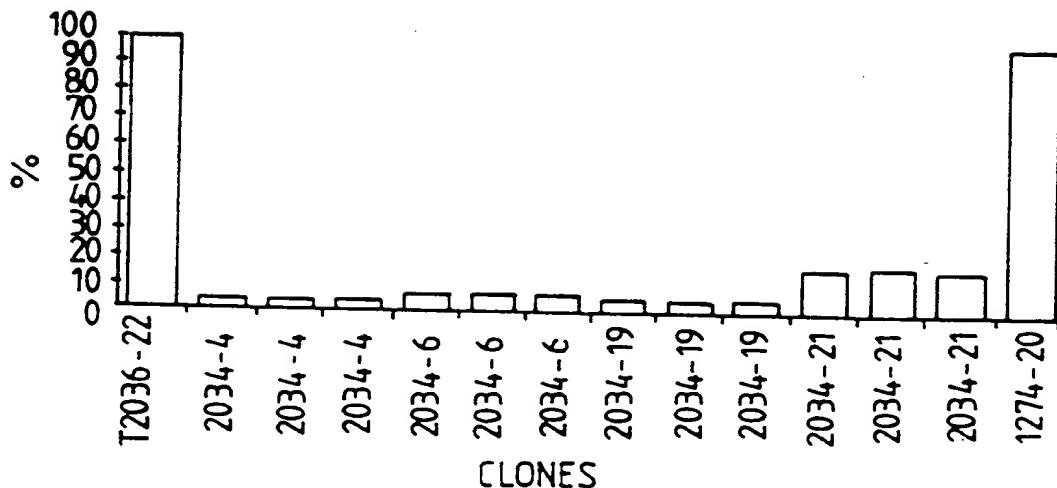


FIG. 5

FIG. 6



14/19

1	TCAGCCGGCCGGCTCCGAGGCAGAGGCTGCATGGAGTGGCCGGCGCGCTCTGGGG	60
-10	M_E_W_P_A_R_L_C_G	9
61	CTGTGGCGCTGCTCTGCAGCCGGCGGGGGCGGGGGCGCCGCCTACG	120
10	L_W_A_L_L_L_C_A_G_G_G_G_G_G_G_A_A_P_T	29
121	GAAACTCAGCCACCTGTGACAAATTGAGTGTCTCTGTTGAAACCTCTGCACAGTAATA	180
30	E_T_Q_P_P_V_T [N_L_S_V] S_V_E_N_L_C_T_V_I	49
181	TGGACATGGAATCCACCCGAGGGAGGCCAGCTCAAATTGAGTCTATGGTATTTAGTCAT	240
50	W_T_W_N_P_P_E_G_A_S_S [N_C_S_L] W_Y_F_S_H	69
241	TTTGGCGACAAACAAGATAAGAAAATAGCTCCGAAACTCGTCGTTCAATAGAAGTACCC	300
70	F_G_D_K_Q_D_K_K_I_A_P_E_T_R_R_S_I_E_V_P	89
301	CtGAATGAGAGGA'T'TGCTGCAAG'TGGGG'CCCAGTG'TAGCACCAATGAGAGTGAGAAG	360
90	L_N_E_R_I_C_L_Q_V_G_S_Q_C_S_T [N_E_S_E] K	109
361	CCTAGCATTGGTTGAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTG	420
110	P_S_I_I_V_F_K_C_I_S_P_I_E_G_D_P_E_S_A_V	129
421	ACTGAGCTTCATGCAT'TGGCACAACTTGAGCTACATGAAGTG'TCTTGGCTCCCTGGA	480
130	T_E_L_Q_C_I_W_H [N_L_S_Y] M_K_C_S_W_L_P_G	149
481	AGGAATACCACTGGACACTAACTATACTCTACTATTGGCACAGAAGCCTGGAAAAAA	540
150	R_N_T_S_P_D_T [N_Y_T_L] Y_Y_W_H_R_S_L_E_K	169
541	ATTCATCAATGTGAAAACATCTTAGAGAAGGCCAATACTTGGTTGTTCCCTTGATCTG	600
170	I_H_Q_C_E_N_I_F_R_E_G_Q_Y_F_G_C_S_F_D_L	189
601	ACCAAAGTGAAGGATTCCAGTTTGAAACAACACAGTGTCCAATAATGGTCAAGGATAAT	660
190	T_K_V_K_D_S_S_F_E_Q_H_S_V_Q_I_M_V_K_D_N	209
661	GCAGGAAAAATTAAACCATTCAATATAGTGCCTTAACCTCCGTGTGAAACCTGAT	720
210	A_G_K_I_K_P_S_F_N_I_V_P_L_T_S_R_V_K_P_D	229
721	CCTCCACATATTAAACCTCTCCTCCACAATGATGACCTATATGTGCAATGGAGAAT	780
230	P_P_H_I_K [N_L_S_F] H_N_D_D_L_Y_V_Q_W_E_N	249
781	CCACAGAATTATTAGCAGATGCCATTGGTAAAGTAGAAGTCATAAACAGCCAAACT	840
250	P_Q_N_F_I_S_R_C_L_F_Y_E_V_E_V [N_N_S_Q] T	269
841	GAGACACATAATGTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTGAGAGA	900
270	E_T_H_N_V_F_Y_V_Q_E_A_K_C_E_N_P_E_F_E_R	289
901	AATGTGGAGAATACATCTGTTCATGGCCCTGGTGTCTCCTGATACATTGAAACACA	960
290	N_V_E [N_T_S_C] F_M_V_P_G_V_L_P_D_T_L_N_T	309
961	GTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAAT	1020
310	V_R_I_R_V_K_T_N_K_L_C_Y_E_D_D_K_L_W_S [N]	329
1021	TGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTA	1080
330	W_S_Q_E_M_S_I_G_K_K_R [N_S_T_L] Y_I_T_M_L	349
1081	CTCATGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTACCTAAAAGG	1140
350	L_I_V_P_V_I_V_A_G_A_I_I_V_L_L_Y_L_K_R	369
1141	CTCAAGATTATTATTCCTCCAATTGATCCTGGCAAGATTAAAGAAATGTT	1200
370	L_K_I_I_I_F_P_P_I_P_D_P_G_K_I_F_K_E_M_F	389
1201	GGAGACCAGAATGATGACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACC	1260
390	G_D_Q_N_D_D_T_L_H_W_K_K_Y_D_I_Y_E_K_Q_T	409
1261	AAGGAGGAAACCGACTCTGAGTGTGATAGAAAACCTGAAGAAGCCTCTCAGTGATGG	1320
410	K_E_E_T_D_S_V_V_L_I_E_N_L_K_K_A_S_Q *	429

FIG.7a

15/19

1381	TATCTGGGAACTTATTAAATGGAAACTGAAACTACTGCACCATTAAAAACAGGCAGCTC	1440
1441	ATAAGAGCCACAGGTCTTATGTTGAGTCGCGCACGAAAAACTAAAAATAATGGCGCT	1500
1501	TTGGAGAAGAGTGTGGAGTCATTCTCATTGAATTATAAAAGCCAGCAGGCTCAAAC	1560
1561	GGGACAAAGCAAAAGTGTGATGAGTGGTGGAGTTAATCTTATCAAGAGTTGTGACA	1620
1621	TCCTGAGGGATCTATACTTGTCTTGTGTCACATGAACAAATTATTTGT	1680
1681	AGGGGAACTCATTGGGGTCAAATGCTAATGTCAAACTTGAGTCACAAAGAACATG	1740
1741	AAAACAAAATGGATAAAATCTGATATGTATTGTTGGATCTATTGAACCATGTTGTG	1800
1801	GCTATTAAAACCTTTAACAGTCGGCTGGTCCGGTGGCTACGCCGTAACTCCAG	1860
1861	CAATTGGGAGTCGGAGGGCGGATCACTCGAGGTCAAGGAGTTCCAGACAGCCTGAC	1920
1921	CAAAATGGTAAACCTCTCTACTAAAACACAAAAATTAACTGGGTGTGGCGCG	1980
1981	TGCCTGTAATCCCAGCTACTCGGGAAAGCTGAGGCAGGTGAATTGTTGAAAC	2040
2041	GGAGGTTGCAGTGAGCAGAGATCACACCACTGCACTCTAGCCTGGGTGACAGAG	2100
2101	TCTGTCTAAAAACAAAACAAAACAAAACAAAAACAAAAACCTCTTAATATTCTG	2160
2161	CATCATTCCTCTCGACAGCATTCTGCTGTTGAAAGCCCCAGAAATCAGTGTGCGC	2220
2221	ATGATGACAACACTACAGAAAAACAGAGGCAAGCTCTTGCCAAGACCTTCAAGC	2280
2281	TTAGGCTGTTAGGGCAGTGGAGGTAAATGACTCCTGGTATTAGAGTTCAACC	2340
2341	AAGTCTCTAACATGTTCTTACCTCTGCTACTCAAGTAGCATTTACTGTGCTTT	2400
2401	GGTTTGTGCTAGGCCCCGGGTGTGAAGCAGACAGACCCCTCCAGGGTTACAGT	2460
2461	TGAGACTCCTCAGTTCTGCCACTTTTTTAATCTCCACCAAGTCATTTCAGAC	2520
2521	TTAACCTCCTCAATTCCAAACACTGATTCCCTTTGCATTCTCCCTCCCTCCTT	2580
2581	GTAGCCTTTGACTTTCATTGAAATTAGGATGTAATCTGCTCAGGAGACCTGGAG	2640
2641	CAGAGGATAATTAGCATCTCAGGTTAAGTGTGAGTAATCTGAGAAACAAATG	2700
2701	TGCATATTGTAACCTCAATGTGAGGGTTTCAGCATTGATATTGTCATTCTAAA	2760
2761	CAGAGATGAGGGTGTACCGTAGAACATTGGTATTGCTTGAGAAAAAAAGAATAG	2820
2821	TTGAACCTATTCTCTTACAAGATGGTCCAGGATTCCCTTTCTGCCCCATAA	2880
2881	ATGATTAATTAAATAGCTTTGTGCTTACATTGGTAGCCAGCCAGCAAGCTGT	2940
2941	ATGCTTTGGGGGATATATTGGGTTCCATTCTCACCTATCCACACAACATATCCGT	3000
3001	ATATCCCCTACTCTTACCTTCCACACACAGACTCATATTACTGGTAGGAAC	3060
3061	CCCCACCCATTCTCCTCACACACAGACTCATATTACTGGTAGGAAC	3120
3121	TTATTCCAAGTGTCAAACATTACCAATCATATTAAATACAATGATGCTATTGCA	3180
3181	TCCTGCTCCTAGGGAGGGAGATAAGAACCTCACTCTCACAGGTTGGTACAAGT	3240
3241	GGCAACCTGCTCCATGCCGTGTAGAAGCATGGTCCCTGGCTCTGAGGAAGCTG	3300
3301	GGTTCATGACAATGGCAGATGTAAGTTATTCTGAAGTCAGATTGAGGCTGGAG	3360
3361	CCGTAGTAGATGTTCTACTTGTCTGCTGTTCTAGAAAGAATATTGGTTCTGT	3420
3421	ATAGGAATGAGATTAATTCTCTTCCAGGTATTATAATTCTGGAGCAAAACCATG	3480
3481	CTCCCCCTAGCCATTCTACTGTTATCCTATTAGATGCCATGAAGAGGATGCTG	3540
3541	ATTCCCAACAAACATTGATGCTGACAGTCATGCAGTCAGTCAGTCAGTCAGT	3600
3601	GTTCCCATTCTCTTCTTCTAGCAGTAAAGTGTGAGGGAAAAGGGAGGGAAAAG	3660
3661	TATGGGAATACCTGTGGGGTTGTGATCCCTAGGTCTGGAGCTCTGGAGGTG	3720
3721	ATCAGTGGATTCTCCATCCCTGTGGAAATTAGTAGGCTCATTACTGTTTAGG	3780
3781	GCCTATGTGGATTCTCTAACATACCTAACAGCAAAACCCAGTGTCAAGGATGG	3840
3841	ATTCTTCGTTCAAGTTCTCTCATCTGGCACTGAAGGGATATGTGAAACAA	3900
3901	TGTTAACATTGGTAGTCTCAACCAGGGATTGTTCTGTTAACCTCTTATAGGAA	3960
3961	GCTTGAGTAAAATAATTGTCTTTGTATGTCACCCaaaaaaaaa 4009	

FIG. 7a (continuation)

09/077817

16/19

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FIG. 7b

09/077817

17/19

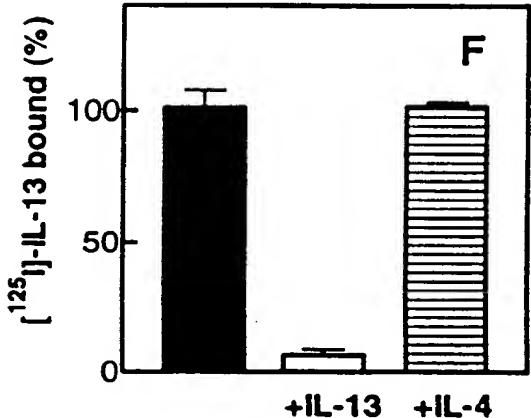
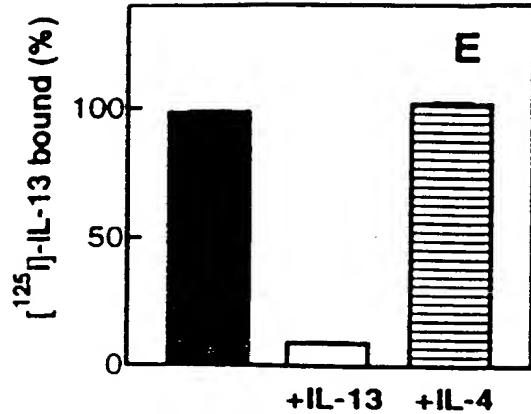
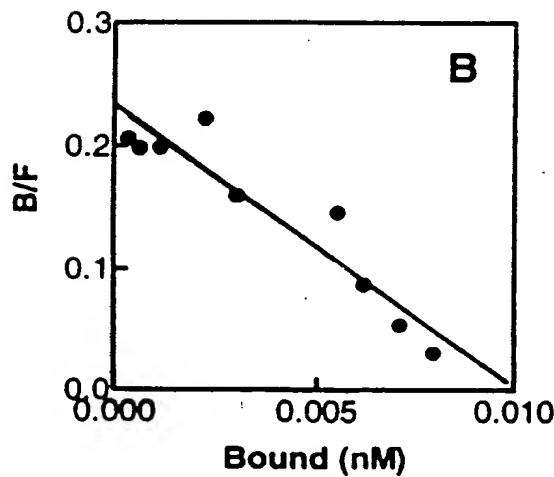
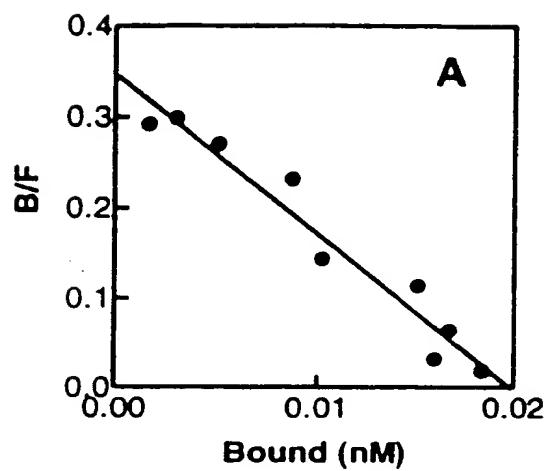


FIG. 8

09/077817

18/19

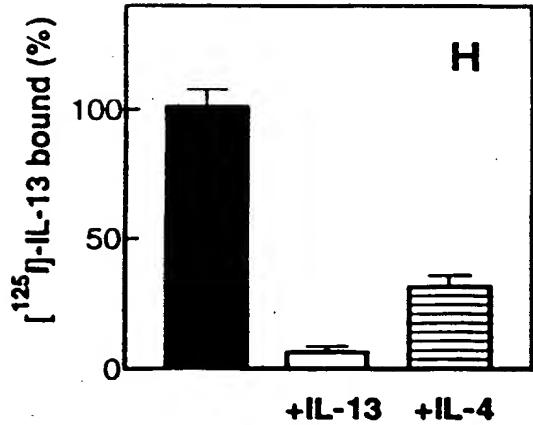
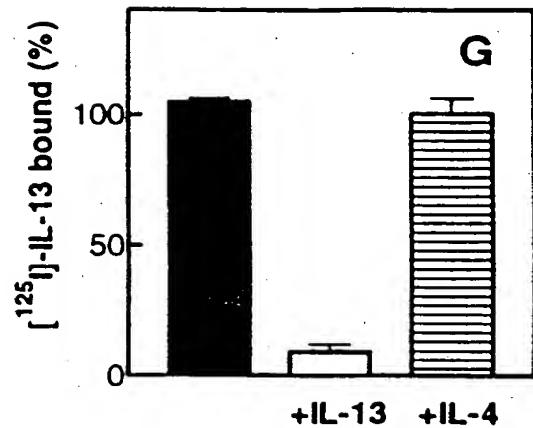
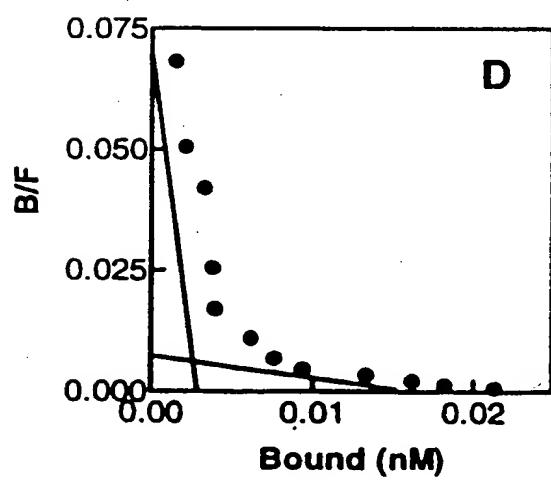
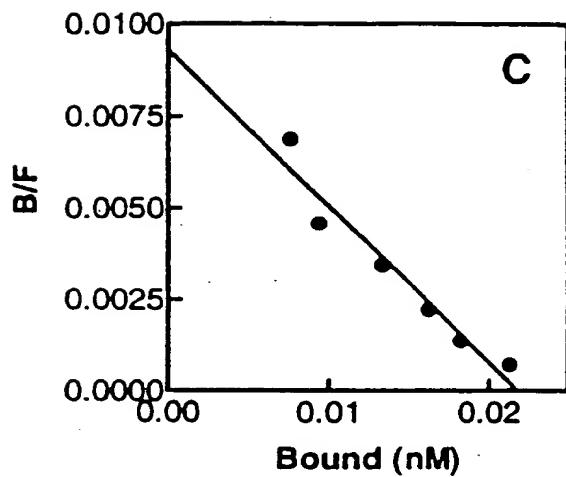


FIG. 8 (continuation)

09/077817

19/19

CHO CHO-4 CHO-13 CHO-4-13
4 13 4 13 c 4 13 c 4 13 c



FIG.9